In the Specification

Please insert the following paragraph on page 1, beginning at line 13:

The Sequence Listing for this application is on duplicate compact discs labeled "Copy 1" and "Copy 2." Copy 1 and Copy 2 each contain only one file named "G-091US04DIV-Subst-Seq-List.doc" which was created on February 11, 2005, and is 397 KB. The entire contents of each of the computer discs are incorporated herein by reference in their entireties.

Please substitute the following paragraph on page 33, beginning at line 26 through to page 34, line 16:

The probes of the present invention are useful for a number of purposes. They can notably be used in Southern hybridization to genomic DNA. The probes can also be used to detect PCR amplification products. They may also be used to detect mismatches in the GENSET gene or mRNA using other techniques. They may also be used to in situ hybridization. Any of the polynucleotides, primers and probes of the present invention can be conveniently immobilized on a solid support. The solid support is not critical and can be selected by one skilled in the art. Thus, latex particles, microparticles, magnetic beads, non-magnetic beads (including polystyrene beads), membranes (including nitrocellulose strips), plastic tubes, walls of microtiter wells, glass or silicon chips, sheep (or other suitable animal's) red blood cells and DURACYTES~~duracytes~~ are all suitable examples. Suitable methods for immobilizing nucleic acids on solid phases include ionic, hydrophobic, covalent interactions and the like. A solid support, as used herein, refers to any material which is insoluble, or can be made insoluble by a subsequent reaction. The solid support can be chosen for its intrinsic ability to attract and immobilize the capture reagent. Alternatively, the solid phase can retain an additional receptor which has the ability to attract and immobilize the capture reagent. The additional receptor can include a charged substance that is oppositely charged with respect to the capture reagent itself or to a charged substance conjugated to the capture reagent. As yet another alternative, the receptor molecule can be any specific binding member which is immobilized upon (attached to) the solid support and which has the ability to immobilize the capture reagent through a

specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid support material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, microparticle, chip, sheep (or other suitable animal's) red blood cells, ~~duracytes®~~ DURACYTES and other configurations known to those of ordinary skill in the art. The polynucleotides of the invention can be attached to or immobilized on a solid support individually or in groups of at least 2, 5, 8, 10, 12, 15, 20, or 25 distinct polynucleotides of the invention to a single solid support. In addition, polynucleotides other than those of the invention may be attached to the same solid support as one or more polynucleotides of the invention.

Please substitute the following paragraph on page 34, beginning at line 33 through to page 35, line 20:

Any polynucleotide provided herein may be attached in overlapping areas or at random locations on the solid support. Alternatively the polynucleotides of the invention may be attached in an ordered array wherein each polynucleotide is attached to a distinct region of the solid support which does not overlap with the attachment site of any other polynucleotide. Preferably, such an ordered array of polynucleotides is designed to be "addressable" where the distinct locations are recorded and can be accessed as part of an assay procedure. Addressable polynucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. The knowledge of the precise location of each polynucleotides location makes these "addressable" arrays particularly useful in hybridization assays. Any addressable array technology known in the art can be employed with the polynucleotides of the invention. One particular embodiment of these polynucleotide arrays is known as the ~~Genechips™~~ GENECHIPS, and has been generally described in U.S. Pat. No. 5,143,854; PCT publications WO 90/15070 and 92/10092, which disclosures are hereby incorporated by reference in their entireties. These arrays may generally be produced using methods known in the art, e.g., Fodor et al., (1991) Science 251:767-777, which disclosure is hereby incorporated by reference in its entirety. The immobilization of arrays of oligonucleotides on solid supports has been rendered possible by the

development of a technology generally identified as "Very Large Scale Immobilized Polymer Synthesis" (VLSIPS™) in which, typically, probes are immobilized in a high density array on a solid surface of a chip. Examples of VLSIPS™ technologies are provided in U.S. Patents 5,143,854; and 5,412,087 and in PCT Publications WO 90/15070, WO 92/10092 and WO 95/11995, which disclosures are hereby incorporated by reference in their entireties. In designing strategies aimed at providing arrays of nucleotides immobilized on solid supports, further presentation strategies known in the art may be used, such as those disclosed in PCT Publications WO 94/12305, WO 94/11530, WO 97/29212 and WO 97/31256, the disclosures of which are incorporated herein by reference in their entireties.

Please substitute the following paragraph on page 44, beginning at line 27:

Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al., (1994), FEBS Letters. 344:191 and in U.S. patent application Ser. No. 08/446,922, which disclosure is hereby incorporated by reference in its entirety. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention. In another example, proteins of the invention are associated by interactions between ~~Flag®~~ FLAG polypeptide sequence contained in fusion proteins of the invention containing ~~Flag®~~ FLAG polypeptide sequence. In a further embodiment, associations proteins of the invention are associated by interactions between heterologous polypeptide sequence contained in ~~Flag®~~ FLAG fusion proteins of the invention and anti-~~Flag®~~ FLAG antibody.

Please substitute the following paragraph on page 69, beginning at line 1:

Sequences derived from polynucleotides of the inventions may be used to isolate the promoters of the corresponding genes using chromosome walking techniques. In one chromosome walking technique, the ~~GenomeWalker™~~ GENOMEWALKER kit available from Clontech is used according to the manufacturer's instructions.

Please substitute the following paragraph on page 101, beginning at line 17 through to page 102, line 15:

Preferred polypeptides for use in the methods of the present invention include the polypeptides of SEQ ID NO:28 comprising the amino acid sequence:
MRLRAQVRLLETRVKQQQVKIKQLLQENEVQFLDKGDENTVVDLGSKRQYADCSEIFN
DGYKLSGFYKIKPLQSPAEFSVYCDMSDGGGWTVIQRRSDGSENFNRGWKDYENGFGX
FVQKHGEYWLGNKNLHFLTTQEDYTLKIDLADFEKNSRYAQYKNFKVGDEKNFYELNI
GEYSGTAGDSLAGNFHPEVQWWASHQRMKFSTWDRDHDNYEGNCAEEDQSGWWFN
RCHXANLNGVYYSGPYTAKTDNGIVWYTWHGWWYSLKSVVMKIRPNDFIPNVI(SEQ ID NO:28); a polypeptide comprising the amino acid sequence of:
MAKVFSFILVTTALIMGREISALEDCAQEQMRLRAQVRLLETRVKQQQVKIKQLLQENE
VQFLDKGDEDTVVDLGSKRQYADCSEIFNDGYKLSGFYKIKPLQSPAEFSVYCDMSDGG
GWTVIQRRSDGSENFNRGWKDYENGFGNFVQKHGEYWLGNKNLHFLTTQEDYTLKIDL
ADFEKNSRYAQYKNFKVGDEKNFYELNIGEYSGTAGDSLAGNFHPEVQWWASHQRMK
FSTWDRDHDNYEGNCAEEDQSGWWFNRCHSANLNGVYYSGPYTAKTDNGIVWYTWH
GWWYSLKSVVMKIRPNDFIPNVI(SEQ ID NO:113); a polypeptide comprising the amino acid sequence of:
SPISNCEITITDPGKFYNSNSVFSRGNMAKVFSFILVTTALXMGREISALEDCAQEQMRLR
AQVRLLETRVKQQQVKIKQLLQENEVQFLDKGDENTVVDLGSKRQYADCSEIFNDGYK
LSGFYKIKPLQSPAEFSVYCDMSDGGGWTVIQRRSDGSENFNRGWDYENGFGNFVQKH
GEYWLGNKNLHFLTTQEDYTLKIDLADFEKNSRYAQYKNFKVGDEKNFYELNIGEYSGT
AGDSLAGNFHPEVQWWASHQRMK FSTWDRDHDNYEGNCAEEDQSGWWFNRCHSA
NLNGVYYSGPYTAKTDNGIVWYTWHGWWY SLKSVVMKIR PNDFIPNVI(SEQ ID NO:114); a polypeptide comprising the amino acid sequence of:
MAKVFSFILVTTALIMGREISALEDCAQEQMRLRAQVRLLETRVKQQQVKIKQLLQENE
VQFLDKGDENTVVDLGSKRQYADCSEIFNDGYKLSGFYKIKPLQSPAEFSVYCDMSDGG
GWTVIQRRSDGSENFNRGWKDYENGFGNFVQKHGEYWLGNKNLHFLTTQEDYTLKIDL
ADFEKNSRYAQYKNFKVGDEKNFYELNIGEYSGTAGDSLAGNFHPEVQWWASHQRMK
FSTWDRDHDNYEGNCAEEDQSGWWFNRCHSANLNGVYYSGPYTAKTDNGIVWYTWH

GWWYSLKSVVMKIRPNDFIPNVI (SEQ ID NO:115); and a polypeptide comprising the amino acid sequence of:

MKLANWYWLSSAVLATYGFLVVANNETEEIKDERAKDVCPVRLESRGKCEEAGECPYQ VSLPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPST GAPGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLVNMNNIENYVDSKVA NLTFVVNSLDGKCSKCPSQEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTPDPKNSSFE VYCDMETMGGGWTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSK EMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLK FFTTPDKDNDRYPSGNCGLYYSSGWWFDACLSANLNGKYYHQKYRGVRNGIFWGTWP GVSEAHPGGYKSSFKEAKMMIRPKHFKP (SEQ ID NO:227). Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 102, beginning at line 20:

The polynucleotides of SEQ ID NOs:9, 11, 13 and 15 and the polypeptides of SEQ ID NOs:10, 12, 14, and 16, respectively, encode the soluble Low density lipoprotein receptor-Related Protein-10 (sLRP10)

MSASCCLSWCPAKAKSKCGPTFFPCASGIHCIIGRFRCNGFEDCPDGSDEENCTANPLLCS TARYHCKNGLCIDKSFICDGQNNCQDNSDEESCESSQAIFPQITVS (SEQ ID NO:116). Preferred polynucleotides and polypeptides of the invention comprise the nucleic acid sequences of SEQ ID NOs:9, 11, 13, and 15 and amino acid sequences of SEQ ID NOs:10, 12, 14, and 16. It will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NOs:9, 11, 13, and 15 and polypeptides of SEQ ID NOs:10, 12, 14, and 16 described throughout the present application also pertain to the human cDNAs of Clones 147103_106-024-1-0-H6-F, 224168_116-096-3-0-G11-F, 243303_116-118-4-0-A3-F, and 225432_116-083-3-0-C6-F, and the polypeptides encoded thereby. Preferred compositions of the invention include polynucleotides and polypeptides of Clones 147103_106-024-1-0-H6-F, 224168_116-096-3-0-G11-F, 243303_116-118-4-0-A3-F, and 225432_116-083-3-0-C6-F; SEQ ID NOs:9, 11, 13, and

15; SEQ ID NOs:10, 12, 14, and 16. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 105, beginning at line 30 through to page 106, line 19:

The cDNA of Clone 158523_106-030-2-0-A3-F (SEQ ID NO:19) encodes the OsteoAngioRemodeling (OAR) protein comprising the amino acid sequence MRAWIFFLLCLAGRALAAPQQEALPDETEVVEETVAEVTEVSVGANPVQVEVGEFDDG AEETEEEVVAENPCQNHHCKHGKVCELDENNTPMCVCQDPTSCPAPIGEFEKVCSNDN KTFDSSCHFFATKCTLEGTKKGHKLHLDYIGPCKYIPPCLDSELTEFPLRMRDWLKNVLV TLYERDEDNNLLTEKQKLRVKKIHENEKRLEAGDHPVELLARDCQAVSARKAKIKSEM (SEQ ID NO:20). Accordingly, it will be appreciated that all characteristics and uses of the polypeptides of SEQ ID NO:20 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 158523_106-030-2-0-A3-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:19 described throughout the present application also pertain to the nucleic acids included in Clone 158523_106-030-2-0-A3-F. A preferred embodiment of the invention is directed toward the compositions comprising SEQ ID NO:19, SEQ ID NO:20, or Clone 158523_106-030-2-0-A3-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments. Another preferred embodiment of the invention is directed toward compositions comprising polypeptide fragments of at least six amino acids within SEQ ID NO:20: LLARDCQAVSARK (SEQ ID NO:117), including those having a biological activity described herein, and the corresponding polynucleotides. Preferred polypeptides of the present invention include polypeptide fragments of SEQ ID NO:20 comprising KKIHENEKRLEAGDHPVELLARDCQAVSARKA KIKSEM (SEQ ID NO:118) and the corresponding polynucleotides. Further preferred polypeptides of the present invention include polypeptide ~~fragements~~fragments of SEQ ID NO:20 comprising DYIGPCKYIPPCLDSELTEFPLRMRDWLKNVLVTLYERDEDNNLLTEKQKLRVKKIHENE KRLEAGDHPVELLARDCQAVSARKAKIKSEM (SEQ ID NO:119) and the corresponding

polynucleotides. Polypeptide fragments of SEQ ID NO:20 having a biological activity of those described herein and polynucleotides encoding the same are also included in the invention. Biological activities include increasing bone density when contacted with osteoblasts, tissue remodeling, and wound healing.

Please substitute the following paragraphs on page 110, beginning on line 3 through to page 111, line 9:

In an embodiment, Armapoptin polynucleotides are used in a method of gene therapies to restore cell-cell adhesion and to promote caspase-dependent apoptosis, preferably in epithelial cell-based tumors including breast carcinoma, ovarian carcinoma, lung carcinoma, non-small cell lung carcinoma (NSCLC), and squamous cell carcinoma of head and neck (SCCHN). Preferred compositions of Armapoptin to be used in methods of gene therapy, further referred to as "gene therapy compositions of Armapoptin" are compositions comprising the full-length DNA, SEQ ID NO:29, or fragments thereof, encoding a polypeptide or fragments thereof, including the sequences

aatcctagtcttcgtttggtccggttgcactcttcctatagcccagagggcgagagggcctgtggcctgggggaaggaggacgaggttctgc
ctggatcccagcaggacgctgtgccatttgggaacaaaggaatagtctgcctggaatccctgcagatcttggggccggaggccagtccaac
ccttggagcaggaagaaacgcaaagttgtcaagaaccaagtcgagctgcctcagagccggcccgcagtagctgcagactccgcccgcga
cgtgtgcgcgcttctctgggccagagcgagcctgttttgtgctcgggttaagagatttgtcccagctataccgcgtggccgctggtgtggttatc
ggggctggtgcctgctactgtgtatacagactggcttggggaagagacgagaacgagaaaatctgggacgaagacgaggagtctaggac
acctcakagattggggttgagactgtgaaaggagctaaaactaacgctggggcagggtctggggccaaacttcagggtgattcagaggtca
agcctgaggtgagtttgggactcgaggattgtccgggtgtaaaagagaaggcccattcaggatcccacagcggaggtggcctagaggcca
aggccaaggccctttcaacacgctgaaggaacaggcaagtgcaaaggcaggcaaaggggctagggtgggaccatctctgggaacagg
acccttgcaccgagtttaccctgcccaggaggcaggggtggaggctgccaccccaccaggagtggatctagggccgggggcagggcaa
gtggaaaatccaagggaaaggcccgaagtaagagcaccagggctccagctacaacatggcctgtccggagaggcaagttcaactttcctta
taaaattgatgatattctgagtgctcccgacctccaaaaggtcctcaacatcctggagcgaacaaatgatccttttattcaagaagtagccttggt
cactctgggtaacaatgcagcatattcatttaaccagaatgccatacgtgaattgggtggtgtcccaattattgcaaaaaaaaaaaaaaa
(SEQ ID NO:120),

or

tctgagtacc agctccccac tgccctgagg gcgggccggc ctgcggcgga gggaaaaaggaagaggagaa ggaaattgtc ccgaatccct gcagtgggtc caagcctctc ccgggtggccagtctttctg taggttgcgg cacaacgcca ggcaaaagaa gaggaaggaa tttaatcctaatcggtggag gtcgatttga gggtctgctg tagcaggtgg ctccgcttga agcgagggaggaagtttcct ccgatcagta gagattggaa agattgttgg gagtggcacaccactagggaaaagaagaag gggcgaactg cttgtcttga ggaggtcaac ccccacaatc agctcttgtggccttgaagt ggctgaagac gatcaccctc cacaggcttg agcccagtcc cacagccttcctcccccagc ctgagtgact actctattcc ttggtccctg ctattgtcgg ggacgattgcatgggctacg ccaggaaagt aggctgggtg accgcaggcc tggtgattgg ggctggcgcctgctattgca tttatagact gactagggga agaaaacaga acaaggaaaa aatggctgagggtggatctg gggatgtgga tgatgctggg gactgttctg gggccaggta taatgactggtctgatgatg atgatgacag caatgagagc aagagtatag tatggtaccc accttgggctcggattggga ctgaagctgg aaccagagct agggccaggg caagggccag ggctacccgggcacgtcggg ctgtccagaa acgggcttcc cccaattcag atgataccgt tttgtcccctcaagagctac aaaaggttct ttgcttggtt gagatgtctg aaaagcctta tattcttgaagcagctttaa ttgctctggg taacaatgct gcttatgcat ttaacagaga tattattcgtgatctgggtg gtctcccaat tgtcgcaaag attctcaata ctcgggatcc catagttaaggaaaaggctt taattgtcct gaataacttg agtgtgaatg ctgaaaatca gcgcaggcttaaagtataca tgaatcaagt gtgtgatgac acaatcactt ctcgcttgaa ctcatctgtgcagcttgctg gactgagatt gcttacaaat atgactgtta ctaatgagta tcagcacatgcttgctaatt ccatttctga ctttttcgt ttattttcag cgggaaatga agaaaccaaacttcaggttc tgaaactcct tttgaatttg gctgaaaatc cagccatgac tagggaactgctcagggccc aagtaccatc ttcactgggc tccctcttta ataagaaaga gaacaaagaagttattctta aacttctggt catatttgag aacataaatg ataatttcaa atgggaagaaaatgaaccta ctcagaatca attcggtgaa ggttcacttt ttttcttttt aaaagaatttcaagtgtgtg ctgataaggt tctgggaata gaaagtcacc atgatttttt ggtgaaagtaaaagttggaa aattcatggc caaacttgct gaacatatgt tcccaaagag ccaggaataacaccttgatt ttgtaattta gaagcaacac acattgtaaa ctattcattt tctccaccttgtttatatgg taaaggaatc ctttcagctg ccagttttga ataatgaata tcatattgtatcatcaatgc tgatatttaa ctgagttggt ctttaggttt aagatggata aatgaatatcactacttgtt ctgaaaacat gtttgttgct ttttatctcg ctgcctagat tgaaatattttgctatttct tctgcataag tgacagtgaa ccaattcatc atgagtaagc tcccttctgtcattttcatt gatttaattt gtgtatcatc aataaaattg tatgttaatg ctggaagggaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa (SEQ ID NO:121).

Please substitute the following paragraph on page 112, beginning at line 3:

Further embodiments include putative death effector domains for therapeutic use in caspase-dependent cell death including incubation of carcinoma cells with compositions comprising polypeptides of preferred sequences comprising RLAWGRDENEKIWDEDEES

(SEQ ID NO:122) and FADD (SEQ ID NO:226) DED-related domains as described in Eberstadt, et al., Nature.392:941-945, 1998, and Hackam, et al., J.Biol.Chem.275:41299-41308, 2000, which disclosures are hereby incorporated by reference in their entireties, with the consensus sequence
SSYRVLLLLISEELDSEELEVLLFLCNDDIPKRKLEIKTALDLFSALEEQGLLSEDNLSLLAELL
YRLRRLDLLRRLFG(SEQ ID NO:123).

Please substitute the following paragraph on page 112, beginning at line 24 through to page 113, line 1:

The death effector domain causes neuronal cell death in Huntington's disease (Hackam, et al., J. Biol. Chem. 275:41299-41308, 2000, which disclosures are hereby incorporated by reference in their entirety) by stronger association with the mutant, glutamine rich protein, which causes the disease as opposed to wild-type huntingtin in healthy individuals. Another embodiment uses Armapoptin and ALEX-1, partial sequences thereof including the death effector domain RLAWGRDENEKIWDEDEES, and the death effector domain of the huntingtin-interacting protein (HIP-1), conserved among related sequences with the consensus peptide
SSYRVLLLLISEELDSEELEVLLFLCNDDIPKRKLEIKTALDLFSALEEQGLLSEDNLSLLAE
LLYRLRRLDLLRRLFG(SEQ ID NO:123) for competitive binding studies with wild-type huntingtin and the disease-causing mutant. By contacting polypeptides of the invention with wt- and mt- (glutamine-rich) huntingtin, peptide-protein interactions will be analyzed by biophysical methods and validated using the following steps as described in Scalley, et al., Biochemistry. 38:15927-15935, 1999; Chaillan-Huntington et al., ~~J Biol Chem.~~J. Biol. Chem. 275:5874-5879, 2000; Lohner et al., Biochim Biophys Acta.1462:141-156, 1999; Eberstadt, et al., Nature 392:941-945, 1998, which disclosures are hereby incorporated in their entireties.

Please substitute the following paragraph on page 113, beginning at line 6:

Structure determination of polypeptide/huntingtin complexes by NMR and X-ray crystallography. Co-incubation of cell lines like 293 T cells with protein-peptide complexes, and

co-transfection of cells with wt- and mt-huntingtin- encoding plasmids and cloned oligonucleotides for cytotoxicity assays as well known in the art.

Another embodiment includes the method to use armadillo repeats of armapoptin, including NFPYKIDDILSAPDLQKVLNILERTNDPFIQEVALVTLGNNAA(SEQ ID NO:124), and YSFNQNAIRELGGVPIIAKLIKTKDPIIREKTYNALNNLSV(SEQ ID NO:125) as single repeats, and naturally occurring tandem array repeats NFPYKIDDILSAPDLQKVLNILERTNDPFIQEVALVTLGNNAAYSFNQNAIRELGGVPIIAK LIKTKDPIIREKTYNALNNLSV (SEQ ID NO:126) for the restoration of cell-cell adhesion in treatment or prevention of cancer or other diseases or disorders where restoration of cell-cell adhesion is sought, wherein said method includes contacting cells in need of cell-cell adhesion with either monomers or concatamerized forms, either recombinantly or nonrecombinantly, such as dimmers, trimers, or longer repeats, in a cell-cell adhesion restorative amount of an Armapoptin polypeptide of the present invention.

Please substitute the following paragraph on page 121, beginning at line 17 through to page 122, line 12:

The cDNA of Clone 229633_253-2-5-2-A11-F (SEQ ID NO:17) encodes the STAM-SAPper (STAMSAP) protein comprising the amino acid sequence: MDRALQVLQSIDPTDSKPDSQDLLDLEDICQQMGPMIDEKLEEIDRKHSELSELNVKVLE ALELYNKLVNEAPVYSVYSKLHPPAHYPPASSGVPMQTYPVQSHGGNYMGQSIHQVTV AQSYSLGPDQIGPLRSLPPNVNSSVTAQPAQTSYLSTGQDTVSNPTYMNQNSNLQSATGT TAYTQQMGMSVDMSSYQNTTSNLPQLAGFPVTVPAHPVAQQHTNYHQQPLL (SEQ ID NO:18). Accordingly, it will be appreciated that all characteristics and uses of the polypeptides of SEQ ID NO:18 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 229633_253-2-5-2-A11-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:17 described throughout the present application also pertain to the nucleic acids included in Clone 229633_253-2-5-2-A11-F. A preferred embodiment of the invention is directed toward the compositions comprising SEQ ID NO:17, SEQ ID NO:18, and Clone 229633_253-2-5-2-A11-F.

Another preferred embodiment of the invention is directed toward compositions comprising polynucleotide fragments of at least eighteen contiguous nucleotides selected from: gagcaagacgtggtgatgccaattggtggaaaggagaaaatcac (SEQ ID NO:127), preferably those polynucleotides that encode for polypeptides having a biological activity described herein. Further preferred polynucleotides of the present invention include nucleic acids comprising: gaagcggmgsggtctagggagccgcggccgcgggtcacccggcgggtagcagttgctgagtgtcagctagacagcagcgactagggct cgggcgccggcgagatgcctttgttcaccgccaacccccttcgagcaagacgtggtgatgccaattggtggaaaggagaaaatcac (SEQ ID NO:128) preferably those that encode for polypeptides having a biological activity described herein. Further preferred polynucleotides of the present invention include nucleic acids of SEQ ID NO:17 comprising gaagcggmgsggtctagggagccgcggccgcgggtcacccggcgggtagcagttgctgagtgtcagctagacagcagcgactagggct cgggcgccggcgagatgcctttgttcaccgccaacccccttcgagcaagacgtggtgatgccaattggtggaaaggagaaaatcacagagg aataggacttttcccatccaattttgtaacaactaatttaaacatagagactgaggcagcggctgtggacaaattgaatgtaattgatgatgatgt ggaggaaattaagaaatcagagcctgagcctgtttatatagatgaggataagatggatagagccctgcaggtacttcagagtatagatccaac agattcaaaaccagactcccaagacctttggatttagaagatatctgccaaca (SEQ ID NO:129) preferably those that encode for polypeptides of having a biological activity described herein. Polypeptides of the invention having a biological activity of x%, where x is any integer between 1 and 100 of those described herein and polynucleotides encoding the same are also included in the invention. Polypeptides of the invention with biological activity are defined as polypeptides that can be phosphorylated by a tyrosine kinase such as a Janus kinase (Jak).

Please substitute the following paragraphs on page 128, beginning at line 35 through to page 129, line 19:

The cDNA of clone 1000848582_181-40-4-0-A11-F (SEQ ID NO:3) encodes the protein of SEQ ID NO:4 comprising the amino acid sequence MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYY ATNSCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDN PVGTGFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAA GIGLELYKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVA

EQVLNAVNKGLYREATELWGKAEMIIEQVKRGNTQRLACLAFSGGYRAHGWCCQTWS
LH (SEQ ID NO:4). Accordingly it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:4 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 1000848582_181-40-4-0-A11-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:3 described throughout the present application also pertain to the nucleic acids included in Clone 1000848582_181-40-4-0-A11-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:3, SEQ ID NO:4, and Clone 1000848582_181-40-4-0-A11-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

The protein of SEQ ID NO:4 encodes a novel serine carboxypeptidase designated here serine carboxypeptidase hx (SCPhx). SCPhx has a unique C-terminal sequence of 31 amino acids comprising KRGNTQRLACLAFSGGYRAHGWCLQTWSLH (SEQ ID NO:130). This unique sequence within SCPhx contributes the histidine of the catalytic triad. SCPhx cleaves the peptide bond between the penultimate and C-terminal amino acid residues of its protein or peptide substrate and, in so doing, can either activate or inactivate the biological function of the substrate.

Please substitute the following paragraph on page 131, beginning at line 10:

The cDNA of clone 1000770704_208-27-3-0-G6-F (SEQ ID NO:7) encodes the protein of SEQ ID NO:8 comprising the amino acid sequence
MRLPAQLLGLLMLWVSGSSGDIVMTQSPLFLPVTPGEPASISCRSSQSLLHVQGSNYLDW
YHQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQT
PFTFGPGTRVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE
C (SEQ ID NO:8). Accordingly it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:8 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 1000770704_208-27-3-0-G6-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID

NO:7 described throughout the present application also pertain to the nucleic acids included in Clone 1000770704_208-27-3-0-G6-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:7, SEQ ID NO:8, and Clone 1000770704_208-27-3-0-G6-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraphs on page 132, beginning at line 22 through to page 133, line 3:

The cDNA of clone 1000839315_220-26-1-0-F3-F (SEQ ID NO:5) encodes the protein of SEQ ID NO:6 comprising the amino acid sequence: MKFFVFALVLALMISMISADSHEKRHHGYRRKFHEKHHSYHITLLPLFEESSKSNANEKH YNLLYTLCFRILAFSIVT(SEQ ID NO:6). Accordingly it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:6 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 1000839315_220-26-1-0-F3-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:5 described throughout the present application also pertain to the nucleic acids included in Clone 1000839315_220-26-1-0-F3-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:5, SEQ ID NO:6, and Clone 1000839315_220-26-1-0-F3-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

The protein of SEQ ID NO:6 encodes Chimerin, a chimeric polypeptide encoded by an exon derived from the histatin 1 gene spliced downstream onto an exon derived from the linked statherin gene. Specifically, an exon encoding the N-terminal amino acids of both histatin 1 and Chimerin (MKFFVFALVLALMISMISADSHEKRHHGYRRKFHEKHHS(SEQ ID NO:131)) is spliced onto a statherin-derived exon that encodes the novel C-terminal amino acids of Chimerin (YHITLLPLFEESSKSNANEKHYNLLYTLCFRILAFSIVT(SEQ ID NO:132)) but in contradistinction entirely 3'-untranslated nucleotide sequence in statherin mRNA.

Please substitute the following paragraphs on page 133, beginning at line 14:

A preferred embodiment of the invention is directed to compositions comprising the amino acid sequence of SEQ NO:6 (Chimerin)
MKFFVFALVLALMISMISADSHEKRHHGYRRKFHEKHHSYHITLLPLFEESSKSNANEKH
YNLLYTLCFRILAFSIVT(SEQ ID NO:6).

Further included in the invention are fragments of the full-length Chimerin polypeptide having a biological activity described herein as well as the polynucleotides encoding these fragments. Preferred fragments with biological activity include the amino acid sequence comprising
DSHEKRHHGYRRKFHEKHHSYHITLLPLFEESSKSNANEKHYNLLYTLCFRILAFSIVT (SEQ ID NO:133) or
DSHEKRHHGYRR (SEQ ID NO:134) or
KFHEKHHSYHITLLPLFEESSKSNANEKHYNLLYTLCFRILAFSIVT(SEQ ID NO:135).

Please substitute the following paragraph on page 134, beginning at line 24:

In a further preferred embodiment, the present invention provides for an antibody that specifically binds Chimerin. The invention further relates to a method of screening for antibodies that specifically bind Chimerin comprising the steps of contacting the unique C-terminal 39 amino acids of Chimerin
(YHITLLPLFEESSKSNANEKHYNLLYTLCFRILAFSIVTSEQ ID NO:132)) with said test antibody and detecting or measuring whether said test antibody binds said Chimerin polypeptide. Further preferred is a method to use compositions comprising this antibody in diagnostic assays to measure Chimerin concentration in bodily fluids, including saliva.

Please substitute the following paragraphs on page 134, beginning at line 35 through to page 135, line 14:

The cDNA of clone 223583_114-044-2-0-E11-F (SEQ ID NO:1) encodes the protein of SEQ ID NO:2 comprising the amino acid sequence:
MAACQLLLEITTFLRETFSCLPRPRTEPLVASTDHTKMPSQMEHAMETMMFTFHKFAGD

KGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLDQCRDGKVGFQSFFSLIAGLTIA CNDYFVVHMKQKGKK (SEQ ID NO:2). Accordingly it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:2 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 223583_114-044-2-0-E11-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:1 described throughout the present application also pertain to the nucleic acids included in Clone 223583_114-044-2-0-E11-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:1, SEQ ID NO:2, and Clone 223583_114-044-2-0-E11-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

The protein of SEQ ID NO:2 encodes S-100A10 Related Protein (S-100A10rP), which is a splice variant of S-100A. Specifically, the protein of SEQ ID NO:2 encodes the S-100A10 polypeptide preceded by a unique sequence of 37 amino acids at the amino terminus comprising MAACQLLLEITTFLRETFSCLPRPRTEP LVASTDHTK (SEQ ID NO:136).

Please substitute the following paragraph on page 137, beginning at line 2:

The cDNA of Clone 477709_174-8-2-0-C10-F (SEQ ID NO:31) encodes the protein of SEQ ID NO:32 comprising the amino acid sequence :
MAWRGWAQRGWGCGQAWGASVGGRSCEELTAVLTPPQLLGRRFNFFIQQKCGFRKAP RKVEPRRSDPGTSGEAYKRSALIPPVEETVFYPSPYPIRSLIKPLFFTVGFTGCAFGSAAIW QYESLKSRVQSYFDGIKADWLDSIRPQKEGDFRKEINKWWNNLSDGQRTVTGIIAANVL VFCLWRVPSLQRTMIRYFTSNPASKVLCSPMLLSTFSHFSLFHMAANMYVLWSFSSSIVN ILGQEQFMAVYLSAGVISNFVSYVGKVATGRYGPSLGAALKAIIAMDTAGMILGWKFFD HAAHLGGALFGIWYVTYGHELIWKNREPLVKIWHEIRTNGPKKGGGSK (SEQ ID NO:32). Accordingly, it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:32 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 477709_174-8-2-0-C10-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:31 described throughout the present application also pertain to the nucleic acids included in Clone

477709_174-8-2-0-C10-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:31, SEQ ID NO:32, and Clone 477709_174-8-2-0-C10-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 145, beginning at line 6:

The cDNA of Clone 1000769575_208-22-1-0-B2-F (SEQ ID NO:35) encodes the protein of SEQ ID NO:36 comprising the amino acid sequence MGMSSLKLLKYVLFFFNLLFWICGCCILGFGIYLLIHNNFGVLFHNLPSLTLGNVFVIVGSII MVVAFLGCMGSIKENKCLLMSFFILLLIILLAEVTLAILLFVAKGLTDSIHRYHSDNSTKAA WDSIQSFLQCCGINGTSDWTSGPPASCPSDRKVEGCYAKARLWFHSNFFIRGPY (SEQ ID NO:136). Accordingly it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:36 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 1000769575_208-22-1-0-B2-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:35 described throughout the present application also pertain to the nucleic acids included in Clone 1000769575_208-22-1-0-B2-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:35, SEQ ID NO:36, and Clone 1000769575_208-22-1-0-B2-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraphs on page 172, beginning at line 30 through to page 174, line 14:

A preferred embodiment of the invention is directed towards using compositions comprising RET-A-MODULIN and other preferred compositions in a method for inhibiting neoplastic cell growth, killing neoplastic cells and treating cancer. More particularly, the invention concerns methods and compositions to inhibit cellular proliferation of neoplastic cells, induce cytotoxicity in neoplastic cells and kill neoplastic cells (e.g., carcinomas, melanoma, and lymphoid tumors such as acute myelocytic leukemia (AML)), wherein said methods comprises

contacting cells with a proliferation-inhibiting amount of RET-A-MODULIN or other sequences of the invention. The method of suppressing neoplastic cell growth comprises the effects selected from the group consisting of: (a) inhibiting cell growth or proliferation; (b) killing said neoplastic cells; (c) inducing apoptosis in said neoplastic cells; (d) inducing necrosis in said neoplastic cells; (e) preventing or inhibiting neoplastic cell invasion; and (f) preventing or inhibiting neoplastic cell metastasis. In a preferred embodiment, the neoplastic are cancerous or from a tumor. In another aspect of the invention, said neoplastic cells is selected from the group consisting of bladder carcinoma, hepatocellular carcinoma, hepatoblastoma, rhabdomyosarcoma, ovarian carcinoma, cervical carcinoma, lung carcinoma, breast carcinoma, squamous cell carcinoma in head and neck, esophageal carcinoma, thyroid carcinoma, astrocytoma, ganglioblastoma, neuroblastoma, lymphoma, myeloma, sarcoma and neuroepithelioma. In yet another aspect of the invention, said neoplastic cells are malignant or benign. Further included in the invention are the following protein sequences:

MLDSLLALGGLVLLRDSVEWEGRSLLKALVKKSALCGEQVHILGCEVSEEEFREGFDSDI
NNRLVYHDFFRDPLNWSKTEEAFPGGPLGALRAMCKRTDPVPVTIALDSLSWLLLRLPC
TTLCQVLHAVSHQDSCPGDSSSVGKVSVLGLLHEELHGPGPVGALSSLAQTEVTLGGTM
GQASAHILCRRPRQRPTDQTQWFSILPDFSLDLQEGPSVESQPYSDPHIPPVDPTTHLTFNL
HLSKKEREARDSLILPFQFSSEKQQALLRPRPGQATSHIFYEPDAYYDLDQEDPDDDLDI
(SEQ ID NO:137),

MLDSLLAIGGLVLLRDSVEWEGRSLLKALIKKSALRGEQVHVLGCEVSEEEFREGFDSDV
NSRLVYHDLFRDPLNWSKPGEAVPEGPLKALRSMCKRTDHGSVTIALDSLSWLLCHIPC
VTLCQALHALSQQNGDPGDNSLVEQVHVLGLLHEELHGPGSMGALNTLAHTEVTLSGK
VDQTSASILCRRPQQRATYQTWWFSVLPDFSLTLHEGLPLRSELHPDHHTTQVDPTAHLT
FNLHLSKKEREARDSLTLPFQFSSEKQKALLHPVPSRTTGRIFYEPDAFDDVDQEDPDDD
LDI (SEQ ID NO:138),

SLLKALIKKSALRGEQVHVLGCEVSEEEFREGFDSDVNSRLVYHDLFRDPLNWSKPGEA
VPEGPLKALRSMCKRTDHGSVTIALDSLSWLLCHIPCVTLCQALHALSQQNGDPGDNSL
VEQVRVLGLLHEELHGPGSMGALNTLAHTEVTLSGKVDQTSASILCRRPQQRATYQTW
WFSVLPDFSLTLHEGLPLRSELHPDHHTTQVDPTAHLTFNLHLSKKEREARDSLTLPFQFS

SEKQKALLHPVPSRTTGHIFYEPDAFDDVDPEDPDDDLDI (SEQ ID NO:139), MLDSLLAIGGLVLLRDSVEWEGRSLLKALIKKSALRGEQVHVLGCEVSEEEFREGFDSDV NSRLVYHDLFRDPLNWSKPGEAVPEGPLKALRSMCKRTDHGSVTIALDSLSWLLCHIPC VTLCQALHALSQQNGDPGDNSLVEQVHVLGLLHEELHGPGSMGALNTLAHTEVTLSGK VDQTSASILCRRPQQRATYQTWWFSVLPDFSLTLHEGLPLRSELHPDHHTTQVDPTAHLT FNLHLSKKEREARDSLTLPFQFSSEKQKALLHPVPSRTTGRIFYEPDAFDDVDQEDPDDD LDI (SEQ ID NO:138), and MGTPGEGLGRCSHALIRGVPESLASGEGAGAGLPALDLAKAQREHGVLGGKLRQRLGL QLLELPPEESLPLGPLLGDTAVIQGDTALITRPWSPARRPEVDGVRKALQDLGLRIVEMG DENATLDGTDVLFTGREFFVGLSKWTNHRGAEIVADTFRDFAVSTVPVSGSSHLRGLCG MGGPRTVVAGSSEAAQKAVRAMAALTDHPYASLTLPDDAASDCLFLRPGLPGATPFLL HRGGSAEAL (SEQ ID NO:140).

These embodiments also comprise the death effector domain of RET-A-MODULIN, and other death effector domains including peptides LVKKSALCGEQVHIL (SEQ ID NO:141), LVKRHRLATMPPMV (SEQ ID NO:142), LGWLCLLLLPIPLI (SEQ ID NO:143), LHSDSGISVDSQSL (SEQ ID NO:144), LPAGDRLTGIPSHI (SEQ ID NO:145), LLLPLVLRALLVDV (SEQ ID NO:146), LQPGPQLYDVMDAV (SEQ ID NO:147), LDCVRLLLQYDAEI (SEQ ID NO:148), LDCVRLLLQYNAEI (SEQ ID NO:149), LLEQNDLEPGHTEL (SEQ ID NO:150), LLEQNDLERGHTGL (SEQ ID NO:151), MDGPRLLLLLLLGV (SEQ ID NO:152), MDRLRLLLLLILGV (SEQ ID NO:153), LKPENILVDNDFHI (SEQ ID NO:154), LKPENILVDRDFHI (SEQ ID NO: 155), LLLPLVLLELLVGI (SEQ ID NO:156), LLLSLVLLALLMGI (SEQ ID NO:157), LLLSLVLLALLMGI (SEQ ID NO:158), LWALLILLIPIVLI (SEQ ID NO:159), LWLLTILVLLIPLV (SEQ ID NO:160), LLPLPVRAQLCAHL (SEQ ID NO:161), WTELARELDFTEEQIH (SEQ ID NO:162), WRRLARQLKVSDTKID (SEQ ID NO:163), WKRLARELKVSEAKMD (SEQ ID NO:164), WHQLHGKKEAYDTLIK (SEQ ID NO:165), WRQLAGELGYKEDLID (SEQ ID NO:166), WEPMVLSLGLSQTDIY (SEQ ID NO:167), WAELARELQFSVEDIN (SEQ ID NO:168), WAELARELQFSVEDIN

(SEQ ID NO:169), WRHLAGELGYQPEHID (SEQ ID NO:170), WRHLAGELGYQPEHID (SEQ ID NO:171), WKNCARKLGFTQSQID (SEQ ID NO:172), WKNCARKLGFTESQID (SEQ ID NO:173), WKEFVRRLGLSDHEID (SEQ ID NO:174), WKEFMRFMGLSEHEIE (SEQ ID NO:175), WKEFVRRLGLSEHEIE (SEQ ID NO:176), WKEFMRLLGLSEHEIE (SEQ ID NO:177), WKEFVRTLGLREAEIE (SEQ ID NO:178), VKEFVRKNGMEEAKID (SEQ ID NO:179), CWYQSHGKSDAYQDLIK (SEQ ID NO:180), WQQLATAVKLYPDQVE (SEQ ID NO:181).

Please substitute the following paragraph on page 178, beginning at line 26 through to page 179, line 24:

These embodiments comprise methods for detection of RET-A-MODULIN-mediated proliferation inhibition and apoptosis including in vitro activity tests of RET-A-MODULIN or other proteins of the invention or fragments thereof, further cellular proliferation assays, and cellular apoptosis/necrosis assays. Specific examples of apoptosis assays are also provided in the following references. Assays for apoptosis in lymphocytes are disclosed by Noteborn et al., US Patent 5,981,502, 1999, Li et al., "Induction of apoptosis in uninfected lymphocytes by HIV-1 Tat protein", Science 268: 429-431, 1995; Gibellini et al., "Tat-expressing Jurkat cells show an increased resistance to different apoptotic stimuli, including acute human immunodeficiency virus-type 1 (HIV-1) infection", Br. J. Haematol. 89: 24-33, 1995; Martin et al., "HIV-1 infection of human ~~CD4.sup.+~~ $CD4^+$ T cells in vitro. Differential induction of apoptosis in these cells." J. Immunol. 152:330-342, 1994; Terai et al., "Apoptosis as a mechanism of cell death in cultured T lymphoblasts acutely infected with HIV-1", J. Clin Invest. 87: 1710-1715, ~~199 1~~ 1991; Dhein et al., "Autocrine T-cell suicide mediated by APO-1/(Fas/CD95)", Nature 373: 438-441, 1995; Katsikis et al., "Fas antigen stimulation induces marked apoptosis of T lymphocytes in human immunodeficiency virus-infected individuals", J. Exp. Med. 1815:2029-2036, 1995; Westendorp et al., "Sensitization of T cells to CD95-mediated apoptosis by HIV-1 Tat and gp120", Nature 375:497, 1995; DeRossi et al, Virology 198:234-244, 1994. Assays for apoptosis in fibroblasts are disclosed by: Vossbeck et al, "Direct transforming activity of TGF-beta on rat fibroblasts", Int. J. Cancer 61:92-97, 1995; Goruppi

et al., "Dissection of c-myc domains involved in S phase induction of NIH3T3 fibroblasts", Oncogene 9:1537-44, 1994; Fernandez et al, "Differential sensitivity of normal and Ha-ras transformed C3H mouse embryo fibroblasts to tumor necrosis factor: induction of bcl-2, c-myc, and manganese superoxide dismutase in resistant cells", Oncogene 9:2009-2017, 1994; Harrington et al., "c-Myc-induced apoptosis in fibroblasts is inhibited by specific cytokines", EMBO J. 13:3286-3295, 1994; Itoh et al., "A novel protein domain required for apoptosis. Mutational analysis of human Fas antigen", J. Biol. Chem. 268:10932-10937, 1993. In vitro cellular proliferation assays comprise cultured cells such as Jurkat, HepG2, K562, or HeLa, which are treated with RET-A-MODULIN or fragments thereof at concentration ranges for example from 0.5 to 25 ug/mL, and percent decrease in cellular proliferation is measured 24, 48, and 72 hours after treatment. Cellular apoptosis is measured using an apoptosis assay kit such as ~~VYBRANT™~~ VYBRANT Apoptosis Assay Kit #3 (Molecular Probes). After harvesting and washing, cells are stained with a FITC-labeled anti-RET-A-MODULIN antibody and analyzed by FACS according to manufacturer's instructions. Cells will be stained with P1 or DAP1 to detect apoptotic nuclei. DNA fragmentation analysis will be performed by cellular DNA extraction and Southern blot analysis using about 1 ug of DNA and hybridized with randomly primed ^{32}P-labeled chromosomal DNA from said cells, which had not been treated, with RET-A-MODULIN.

Please substitute the following paragraph on page 179, beginning at line 32 through to page 180, line 20:

RET-A-MODULIN also shares homologies with two phosphorylated matrix proteins with the human cytomegalovirus, a pathogenic herpesvirus causing complications in patients with suppressed cellular immune functions and in prenatal infections (Ruger et al., J Virology 61:446-453, 1987, Koretz et al., N.Engl.J.Med.314:801-805, 1986, Bowden et al., N.Engl.J.Med.314:1006-1010, 1986). A preferred embodiment comprises the use of RET-A-MODULIN and fragments thereof including GPGPVGALSSLAQTEVTLG (SEQ ID NO:182), EGPSVESQPYSD (SEQ ID NO:183), EVSEEEFREGFDSDINN (SEQ ID NO:184), TTLCQVLHAVSHQDSCPGDSSSVGKVSVLGLLHEELHGPGPVGALS (SEQ ID NO:185),

GPSVESQPYSD (SEQ ID NO:186), CQVLHAVSH (SEQ ID NO:187),
GKVSVLGLLHEELHGPGPV (SEQ ID NO:188)
for vaccination against Herpesvirus infections, as well as a vaccine preparation against Herpesviruses such as human cytomegalovirus (HCMV) and Kaposi Sarcoma-Associated Herpesvirus/Human Herpesvirus 8, which preparation comprises a RET-A-MODULIN protein or protein part according to the invention and optionally one or more carriers and adjuvants suitable for subunit vaccines. The use of a RET-A-MODULIN protein or protein part as defined above in a process for producing RET-A-MODULIN-specific polyclonal or monoclonal antibodies also falls within the scope of the invention. Vaccination and immunization generally refer to the introduction of a non-virulent agent against which an individual's immune system can initiate an immune response, which will then be available to defend against challenge by a pathogen. The immune system identifies invading "foreign" compositions and agents primarily by identifying proteins and other large molecules that are not normally present in the individual. The foreign protein represents a target against which the immune response is made. A further example is a use of RET-A-MODULIN-specific antibodies according to the invention for passive immunization against Herpesvirus infections, as well as an immunization preparation for passive immunization against Herpesvirus infections, which preparation includes RET-A-MODULIN-specific antibodies according to the invention and optionally one or more carriers and adjuvants suitable for passive immunization preparations.

Please substitute the following paragraph on page 180, beginning at line 32 through to page 181, line 10:

The cDNA of clone 1000855165_205-99-1-0-A5-F (SEQ ID:47) encodes the protein of SEQ ID NO:48 comprising the amino acid sequence:
MIYTMKKVHALWASVCLLLNLAPAPLNADSEEDEEHTIITDTELPPLKLMHSFCAFKADD
GPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTREKPDFCFLEEDPGIC
RGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICEDGPNGXQVDNYGTQLN
AVNNSLTPQSTKVPSLFEFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGCG
GNENNFTSKQECLRACKKGFIQRISKGGLIKTKRKRKKQRVKIAYEEIFVKNM(SEQ ID

NO:48). Accordingly, it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:48 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 1000855165_205-99-1-0-A5-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:47 described throughout the present application also pertain to the nucleic acids included in Clone 1000855165_205-99-1-0-A5-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:47, SEQ ID NO:48, and Clone 1000855165_205-99-1-0-A5-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 182, beginning at line 5:

TFPI-1 is a secreted trivalent Kunitz-type plasma proteinase inhibitor that negatively regulates the initiation of coagulation by producing activated factor X (FXa) feedback inhibition of the catalytic complex of activated factor VII (FVIIa) and TF. The second Kunitz domain of TFPI-1 binds and inhibits FXa, whereas the first Kunitz domain is responsible for the inhibition of FVIIa in the TF-FVIIa complex. The linker region between Kunitz domains 1 and 2 of TFPI-1 is comprised of 20 amino acids (US Patent 5,849,875 which disclosures is hereby incorporated by reference in its entirety): TRDNANRIIKTTLQQEKPDF (SEQ ID NO:189). The function of the third Kunitz domain is unknown, although there is evidence that it contains a heparin binding site. Heparin binding site(s) have also been mapped carboxyl-terminal to the third Kunitz domain.

Please substitute the following paragraphs on page 189, beginning at line 2 through to page 191, line 18:

In yet another preferred embodiment, Tifapinix or fragments thereof are used for in vitro diagnostic methods and reagents. Tifapinix and related sequences may be applied in vitro to any suitable sample that might contain plasmin to measure the plasmin present. The assay must include a Signal Producing System (SPS) providing a detectable signal that depends on the amount of plasmin present. The signal may be detected visually or instrumentally. Possible signals include production

of colored, fluorescent, or luminescent products, alteration of the characteristics of absorption or emission of radiation by an assay component or product, and precipitation or agglutination of a component or product. The component of the SPS most intimately associated with the diagnostic reagent is called the "label". A label may be, e.g., a radioisotope, a fluorophore, an enzyme, a co-enzyme, an enzyme substrate, an electron-dense compound, or an agglutinable particle. A radioactive isotope can be detected by use of, for example, a .gamma. counter or a scintillation counter or by autoradiography. Isotopes which are particularly useful are ~~.sup.3 H~~ ^{3}H, ~~.sup.125 I~~ ^{125}I, ~~.sup.131 I~~ ^{131}I, ~~.sup.35 S~~ ^{35}S, ~~.sup.14 C~~ ^{14}C, and, preferably, ~~.sup.125 I~~ ^{125}I. It is also possible to label a compound with a fluorescent compound. When the fluorescent-labeled compound is exposed to light of the proper wavelength, its presence can be detected. Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde, and fluorescamine. Alternatively, fluorescence-emitting metals, such as ~~.sup.125 Eu~~ ^{125}Eu or other anthanide, may be attached to the binding protein using such metal chelating groups as diethylenetriaminepentaacetic acid or ethylenediamine-tetraacetic acid. The proteins also can be detectably labeled by coupling to a chemiluminescent compound, such as luminol, ~~isolumino~~isoluminol, theromatic acridinium ester, imidazole, acridinium salt, and oxalate ester. Likewise, a bioluminescent compound, such as luciferin, luciferase and aequorin, may be used to label the binding protein. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Enzyme labels, such as horseradish peroxidase and alkaline phosphatase, are preferred. There are two basic types of assays: heterogeneous and homogeneous. In heterogeneous assays, binding of the affinity molecule to analyte does not affect the label; thus, to determine the amount of analyte, bound label must be separated from free label. In homogeneous assays, the interaction does affect the activity of the label, and analyte can be measured without separation. Tifapinix, as a plasmin-binding protein may be used diagnostically in the same way that an antiplasmin antibody is used. Thus, depending on the assay format, it may be used to assay plasmin, or, by competitive inhibition, other substances which bind plasmin. The sample will normally be a biological fluid, such as blood, urine, lymph, semen, milk, or cerebrospinal fluid, or a derivative thereof, or a biological tissue, e.g., a tissue section or homogenate. If the sample is a biological fluid or tissue, it may be taken from a human or other

mammal, vertebrate or animal, or from a plant. The preferred sample is blood, or a fraction or derivative thereof. In a related embodiment, Tifapinix or fragments thereof is immobilized, and plasmin in the sample is allowed to compete with a known quantity of a labeled or specifically labelable plasmin analogue. The "plasmin analogue" is a molecule capable of competing with plasmin for binding to Tifapinix or fragments thereof. It may be labeled already, or it may be labeled subsequently by specifically binding the label to a moiety differentiating the plasmin analogue from plasmin. The phases are separated, and the labeled plasmin analogue in one phase is quantified. In a "sandwich assay", both an insolubilized plasmin-binding agent (PBA), and a labeled PBA are employed. The plasmin analyte is captured by the insolubilized PBA and is tagged by the labeled PBA, forming a tertiary complex. The reagents may be added to the sample in any order. The PBAs may be the same or different, and only one PBA needs to comprise Tifapinix or fragments thereof according to this invention (the other may be, e.g., an antibody). The amount of labeled PBA in the tertiary complex is directly proportional to the amount of plasmin in the sample. The two embodiments described above are both heterogeneous assays. A homogeneous assay requires only that the label be affected by the binding of Tifapinix or fragments thereof to plasmin. The plasmin analyte may act as its own label if Tifapinix or fragments thereof are used as a diagnostic reagent. A label may be conjugated, directly or indirectly (e.g., through a labeled anti-Tifapinix antibody), covalently (e.g., with SPDP) or noncovalently, to the plasmin-binding protein, to produce a diagnostic reagent. Similarly, the plasmin-binding protein may be conjugated to a solid phase support to form a solid phase ("capture") diagnostic reagent. Suitable supports include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, and magnetite. The carrier can be soluble to some extent or insoluble for the purposes of this invention. The support material may have any structure so long as the coupled molecule is capable of binding plasmin.

In yet another preferred embodiment, Tifapinix or fragments thereof are used for in vivo diagnostic uses. Tifapinix or fragments thereof, i.e. a Kunitz domain that binds very tightly to plasmin can be used for in vivo imaging. Radiolabeled Tifapinix may be administered to a human or animal subject, typically by injection, e.g., intravenous or arterial other means of administration such as subcutaneous, intramuscular in a quantity sufficient to permit subsequent dynamic and/or static imaging using suitable radio-detecting devices. The dosage is the smallest amount capable of

providing a diagnostically effective image, and may be determined by means conventional in the art, using known radio-imaging agents as guides. Typically, the imaging is carried out on the whole body of the subject, or on that portion of the body or organ relevant to the condition or disease under study. The radiolabeled binding protein has accumulated. The amount of radiolabeled binding protein accumulated at a given point in time in relevant target organs can then be quantified. A particularly suitable radio-detecting device is a scintillation camera, such as a. gamma. camera. The detection device in the camera senses and records (and optional digitizes) the radioactive decay. Digitized information can be analyzed in any suitable way, many of which are known in the art. For example, a time-activity analysis can illustrate uptake through clearance of the radiolabeled binding protein by the target organs with time. The radioisotope used should preferably be pharmacologically inert, and the quantities administered should not have substantial physiological effect. The binding protein may be radio-labeled with different isotopes of iodine, for example ~~.sup.123 I~~ ^{123}I, ~~.sup.125 I~~ ^{125}I, or ~~.sup.131 I~~ ^{131}I (see, for example, U.S. Pat. No. 4,609,725). The amount of labeling must be suitably monitored.

In applications to human subjects, it may be desirable to use radioisotopes other than ~~.sup. 125 I~~ ^{125}I for labeling to decrease the total dosimetry exposure of the body and to optimize the detectability of the labeled molecule. Considering ready clinical availability for use in humans, preferred radio-labels include: ~~.sup.99m Tc~~ ^{99m}Tc, ~~.sup.67 Ga~~ ^{67}Ga, ~~.sup.68 Ga~~ ^{68}Ga, ~~.sup.90 Y~~ ^{90}Y, ~~.sup.111 In~~ ^{111}In, ~~.sup.113m In~~ ^{113m}In, ~~sup. 123 I~~ ^{123}I, ~~sup. 186 Re~~ ^{186}Re, ~~.sup.188 Re~~ ^{188}Re, or ~~.sup.211 At~~ ^{211}At. Radiolabeled protein may be prepared by various methods. These include radio-halogenation by the chloramine-T or lactoperoxidase method and subsequent purification by high pressure liquid chromatography, for example, see Gutkowska et al in "Endocrinology and Metabolism Clinics of America 16 (1):183, 1987. Other methods of radiolabeling can be used, such as IODOBEADS~~.TM~~. Tifapinix or fragments thereof may also be used to purify plasmin from a fluid, e.g., blood. For this purpose, it is preferably immobilized on an insoluble support. Such supports include those also useful in preparing solid phase diagnostic reagents. Proteins can be used as molecular weight markers for reference in the separation or purification of proteins.

Please substitute the following paragraph on page 192, beginning at line 8:

The cDNA of Clone 588098_184-11-4-0-H4-F (SEQ ID NO:49) encodes the protein of SEQ ID NO:50 comprising the amino acid sequence MPSSVSWGILLLAGLCCLVPVSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLN QPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEK GTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMM KRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDR RSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDE KGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIDXNTKSPLFMGKVVNPTQK(SEQ ID NO:50). Accordingly it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:50 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 588098_184-11-4-0-H4-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:49 described throughout the present application also pertain to the nucleic acids included in Clone 588098_184-11-4-0-H4-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:49, SEQ ID NO:50, and Clone 588098_184-11-4-0-H4-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 198, beginning at line 12:

The cDNA of clone 789749_182-14-3-0-C12-F (SEQ ID NO:53) encodes the protein of SEQ ID NO:54 comprising the amino acid sequence: MHFCGGTLISPEWVLTAAHCLEKSPRPSSYKVILGAHQEVNLEPHVQEIEVSRLFLEPTRK DIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTFGAGLLKEAQLPVIE NKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGPLVCFEKDKYILQGVTSWGLG CARPNKPGVYVRVSRFVTWIEGVMRNN(SEQ ID NO:50).
Accordingly it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:54 described throughout the present application also pertain to the polypeptides encoded by

the nucleic acids included in Clone 789749_182-14-3-0-C12-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:53 described throughout the present application also pertain to the nucleic acids included in Clone 789749_182-14-3-0-C12-F. Also preferred are fragments having a biological activity as described therein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 209, beginning at line 35 through to page 210, line 13:

The cDNA of clone 519757_184-4-2-0-F7-F (SEQ ID NO:55) encodes the human intracellular signaling protein comprising the amino acid sequence: MLEVSDALGGPGRVPGATAGMNGVDTSLLCDLLQALTFLTRNEILCIHDTFLKLCPPGKY YKEATLTMDQVSSLPALRVNPFRDRICRVFSHKGMFSFEDVLGMASVFSEQACPSLKIEY AFRIYDFNENGFIDEEDLQRIILRLLNSDDMSEDLLMDLTNHVLSESDLDNDNMLSFSEFE HAMAKSPDFMNSFRIHFWGC (SEQ ID NO:55) and shares features with the Calcium and Integrin-Binding (CIB)- and the DNA-dependent kinase interacting (KIP) protein. It will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:55 and polypeptides of SEQ ID NO:56, described throughout the present application also pertain to the human cDNA of clone 519757_184-4-2-0-F7-F and polypeptide fragments encoded thereby. Polypeptide fragments having a biological activity described herein and polynucleotides encoding the same are included in the present invention. Related polypeptide sequences included in the present invention are MGQCLRYQMH WEDLEEYQALTFLTRNEILCIHDTFLKLCPPGKYYKEATLTMDQVSSLPALRVNPFRDRI CRVFSHKGMFSFEDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQRIILRLL NSDDMSEDLLMDLTNHVLSESDLDNDNMLSFSEFEHAMAKSPDFMYSFRIRFWGC (SEQ ID NO:228).

Please substitute the following paragraph on page 213, beginning at line 28:

The cDNA of clone (SEQ ID NO:57) encodes the protein of SEQ ID NO:58, comprising the sequence:

MGPPGFKGKTGHPGLPGPKGDCGKPGPPGSTGRPGAEGEPGAMGPQGRPGPPGHVGPP
GPPGQPGPAGISAVGLKGDRGATGERGLAGLPGQPGPPGPQGPPGYGKMGATGMGQQG
IPGIPGPPGPMGQPGKAGHCNPSDCFGAMPMEQQYPPMKTMKGPFG (SEQ ID NO:58).

Please substitute the following paragraph on page 218, beginning at line 20:

The cDNA of SEQ ID NO:59 encodes the protein of SEQ ID NO:60, comprising the sequence:
MCFPKVLSDDMKKLKARMHQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLET
VAAYYEEQHPELTPLLEKERDGLRCRGNRSPVPDVEDPATEEPGESFCDKVMRWFQAM
LQRLQTWWHGVLAWVKEKVVALVHAVQALWKQFQSFCCSLSELFMSSFQSYGAPRGD
KEELTPQKCSEPQSSK (SEQ ID NO:60). Accordingly, it will be appreciated that all characteristics and uses of the polypeptide of SEQ ID NO:60 described throughout the present application also pertain to the polypeptide encoded by the nucleic acids included in clone 422353_145-11-3-0-E7-F. In addition, it will be appreciated that all characteristics and uses of the nucleic acid of SEQ ID NO:59 described throughout the present application also pertain to the nucleic acids included in clone 422353_145-11-3-0-E7-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:59, SEQ ID NO:60, and Clone 422353_145-11-3-0-E7-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 221, beginning at line 29 through to page 222, line 5:

The cDNA of Clone 500715621_204-15-3-0-C6-F (SEQ ID NO:61) encodes the 202 amino acid long polypeptide of SEQ ID NO:62 comprising the amino acid sequence :
MELWGAYLLLCLFSLLTQVTTEPPTQKPKKIVNAKKDVVNTKMFEELKSRLDTLAQEVA
LLKEQQALQTVCLKGTKVHMKCFLAFTQTKTFHESSEDCISRGGTLSTPQTGSENDALYE
YLRQSVGNEAEIWLGLNDMAAEGTWVDMTGARIAYKNWETEITAQPDGGKTENCAVL
SGAANGKWFDKRCRDQLPYICQFGIV (SEQ ID NO:62). Accordingly, it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:62 described throughout the

present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 500715621_204-15-3-0-C6-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:61 described throughout the present application also pertain to the nucleic acids included in Clone 500715621_204-15-3-0-C6-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:61, SEQ ID NO:62, and Clone 500715621_204-15-3-0-C6-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraphs on page 223, beginning at line 2:

Preferred PLCP polypeptides for uses in the methods described below include the polypeptides comprising the amino sequence of:
EPPTQKPKKIVNAKKDVVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLKGTKVHM
KCFLAFTQTKTFHESSEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIWLGLNDMA
AEGTWVDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQLPYI
CQFGIV (SEQ ID NO:190);

A polypeptide comprising the amino acid sequence of:
VCLKGTKVHMKCFLAFTQTKTFHESSEDCISRGGTLSTPQTGSENDALYEYLRQSVGNE
AEIWLGLNDMAAEGTWVDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWF
DKRCRDQLPYICQFGIV (SEQ ID NO:191);

A polypeptide comprising the amino acid sequence of:
VHMKCFLAFTQTKTFHESSEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIWLGLN
DMAAEGTWVDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQ
LPYICQ (SEQ ID NO:192).

Please substitute the following paragraph on page 230, beginning at line 19:

The cDNA of Clone 335752_157-15-4-0-B11-F (SEQ ID NO:65) encodes Novel Calpastatin 2 (NC2) protein of SEQ ID NO:66, comprising the amino acid sequence:
MTVLEITLAVILTLLGLAILAILLTRWARRKQSEMYISRYSSEQSARLLDYEDGRGSRHAY
STQSERSKRDYTPSTNSLALSRSSIALPQGSMSSIKCLQTTEEPPSRTAGAMMQFTAPIPGA

TGPIKLSQKTIVQTLGPIVQYPGSNGRINISQLTSEDLTGAKGRVTSGPQFPNSHHVPENLH GYMNSLSLFSPA (SEQ ID NO:66). Accordingly, it will be appreciated that all characteristics and uses of the polypeptides of SEQ ID NO:66 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 335752_157-15-4-0-B11-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:66 described throughout the present application also pertain to the nucleic acids included in Clone 335752_157-15-4-0-B11-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:65, 66 and Clone 335752_157-15-4-0-B11-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 235, beginning on line 15:

The cDNA of Clone 646607_181-15-2-0-E2-F (SEQ ID NO:67) encodes Benzodiazepine Receptor 2 (BZRP-R2) protein of SEQ ID NO:68, comprising the amino acid sequence: MRLQGAIFVLLPHLGPILVWLFTRDHMSGWCEGPRMLSWCPFYKVLLLVQTAIYSVVGY ASYLVWKDLGGGLGWPLALPLRLYAVQLTISWTVLVLFFTVHNPGLALLHLLLLYGLVV STALIWHPINKLAALLLLPYLAWLTVTSALTYHLWRDSLCPVHQPQPTEKSD(SEQ ID NO:68). Accordingly, it will be appreciated that all characteristics and uses of the polypeptides of SEQ ID NO:68 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 646607_181-15-2-0-E2-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:68 described throughout the present application also pertain to the nucleic acids included in Clone 646607_181-15-2-0-E2-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:67, 68 and Clone 646607_181-15-2-0-E2-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 241, beginning at line 30 through to page 242, line 15:

The cDNA of Clone 229654_114-049-1-0-F12-F (SEQ ID NO:69) encodes the 787 amino acid long polypeptide called LAP of SEQ ID NO:70 comprising the amino acid sequence: MFRLWLLLAGLCGLLASRPGFQNSLLQIVIPEKIQTNTNDSSHEYEQISYIIPIDEKLYTVH LKQRYFLTDNFMIYLYNQGSMNTYSSDIQTQCYYQGNIEEYPDSMVTLSTCSGLRGILQF ENVSYGIEPLESAVEFQHVLHKLKNEDNDIAIFIDRSLKEQPMDDNIFISEKSEPAVPDLFP LYLEMHIVVDKTLYDYWGSDSMIVTNKVIEIVGLANSMFTQFKVTIVLSSLELWSDENKI STVGEADELLQKFLEWKQSYLNLRPHDIAYLLIYMDYPRYLGAVFPGTMCITRYSAGVA LYPKEITLEAFAVIVTQMLALSLGISYDDPKKCQCSESTCIMNPEVVQSNGVKTFSSCSLR SFQNFISNVGVKCLQNKPQMQKKSPKPVCGNGRLEGNEICDCGTEAQCGPASCCDFRTC VLKDGAKCYKGLCCKDCQILQSGVECRPKAHPECDIAENCNGSSPECGPDITLINGLSCK NNKFICYDGDCHDLDARCESVFGKGSRNAPFACYEEIQSQSDRFGNCGRDRNNKYVFCG WRNLICGRLVCTYPTRKPFHQENGDVIYAFVRDSVCITVDYKLPRTVPDPLAVKNGSQC DIGRVCVNRECVESRIIKASAHVCSQQCSGHGVCDSRNKCHCSPGYKPPNCQIRSKGFSIF PEEDMGSIMERASGKTENTWLLGFLIALPILIVTTAIVLARKQLKNWFAKEEEFPSSESKSE GSTQTYASQSSSEGSTQTYAGQTRSESSSQADTSKSKSEDSAEAYTSRSKSQDSTQTQSS SN (SEQ ID NO:70). Accordingly, it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:70 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 229654_114-049-1-0-F12-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:69 described throughout the present application also pertain to the nucleic acids included in Clone 229654_114-049-1-0-F12-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:69, SEQ ID NO:70, and Clone 229654_114-049-1-0-F12-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraphs on page 242, beginning at line 36 through to page 244, line 22:

Structurally, LAP has an N-terminal signal sequence (MFRLWLLLAGLCGLLAS (SEQ ID NO:193)), a prodomain (HLKQRYFLTDNFMIYLYNQGSMNTYSSDIQTQCYYQGNIEEYPDSMVTLSTCSGLRGIL QFENVSYGIEPLESAVEFQHVLHKLKNEDNDIAIFIDRSLKEQPMDDNIFISEKS (SEQ ID NO:194)) that has been shown to maintain the enzyme in an inactive state, followed by a metalloprotease domain (LYLEMHIVVDKTLYDYWGSDSMIVTNKVIEIVGLANSMFTQFKVTIVLSSLELWSDENKI STVGEADELLQKFLEWKQSYLNLRPHDIAYLLIYMDYPRYLGAVFPGTMCITRYSAGVA LYPKEITLEAFAVIVTQMLALSLGISYDDPKKCQCSESTCIMNPEVVQSNGVKTFSSCSLR SFQNFISNVGVKCLQNKP (SEQ ID NO:195)) that is important for proteolysis and contains the zinc-binding catalytic site, a disintegrin-like domain (KPVCGNGRLEGNEICDCGTEAQCGPASCCDFRTCVLKDGAKCYKGLCCKDCQILQSGV ECPKAHPECDIAENCNGSSPEC (SEQ ID NO:196)) that has been demonstrated to bind integrins, a cystein-rich region (GLSCKNNKFICYDGDCHDLDARCESVFGKGSRNAPFACYEEIQSQSDRFGNCGRDRNN KYVFCGWRNLICGRLVCTYPTRKPFHQENGDVIYAFVRDSVC (SEQ ID NO:197)) that also have adhesion activity, an EGF-like domain (CDIGRVCVNRECVESRIIKASAHVCSQQCSGHGVCDSRNKCHCSPGYKPPNC (SEQ ID NO:198)) important for substrate recognition, a transmembrane domain (TWLLGFLIALPILIVTTAIVL (SEQ ID NO:199)) and a cytoplasmic tail (ARKQLKNWFAKEEEFPSSESKSEGSTQTYASQSSSEGSTQTYAGQTRSESSSQADTSKS KSEDSAEAYTSRSKSQDSTQTQSSSN (SEQ ID NO:200)) that has been shown in many ADAMs to contain SH3 binding sites and which might be important for cell signaling.

Interestingly, the cytoplasmic C-terminal domain of the LAP protein does not contains any SH3 binding sites but it ends by a 69 amino acid region rich in serine/threonine residues (36% of serine residues; SSESKSEGSTQTYASQSSSEGSTQTYAGQTRSESSSQADTSKSKSEDSAEAYTSRSKSQDS

T QTQSSS (SEQ ID NO:201)).

LAP contains both a disintegrin-like and a metalloprotease domain, and has both cell adhesion and protease activities. However, LAP lacks the catalytic site consensus sequence in its metalloprotease domain (QMLALSLGISYD (SEQ ID NO:202)). LAP, like fertilin beta another catalytically inactive protease, is processed on the sperm cell surface during sperm maturation in the epididymus yielding mature protein that retains disintegrin domain on fertilization-competent sperm.

Preferred LAP polypeptides for uses in the methods described below include the polypeptides comprising the amino sequence of:
KPVCGNGRLEGNEICDCGTEAQCGPASCCDFRTCVLKDGAKCYKGLCCKDCQILQSGV
ECRPKAHPECDIAENCNGSSPECGPDITLINGLSCKNNKFICYDGDCHDLDARCESVFGK
GSRNAPFACYEEIQSQSDRFGNCGRDRNNKYVFCGWRNLICGRLVCTYPTRKPFHQENG
DVIYAFVRDSVCITVDYKLPRTVPDPLAVKNGSQCDIGRVCVNRECVESRIIKASAHVCS
QQCSGHGVCDSRNKCHCSPGYKPPNCQIRSKGFSIFPEEDMGSIMERASGKTENTWLLGF
LIALPILIVTTAIVLARKQLKNWFAKEEEFPSSESKSEGSTQTYASQSSSEGSTQTYAGQTR
SESSSQADTSKSKSEDSAEAYTSRSKSQDSTQTQSSSN (SEQ ID NO:203);

A polypeptide comprising the amino acid sequence of:
KPVCGNGRLEGNEICDCGTEAQCGPASCCDFRTCVLKDGAKCYKGLCCKDCQILQSGV
ECRPKAHPECDIAENCNGSSPECGPDITLINGLSCKNNKFICYDGDCHDLDARCESVFGK
GSRNAPFACYEEIQSQSDRFGNCGRDRNNKYVFCGWRNLICGRLVCTYPTRKPFHQENG
DVIYAFVRDSVCITVDYKLPRTVPDPLAVKNGSQCDIGRVCVNRECVESRIIKASAHVCS
QQCSGHGVCDSRNKCHCSPGYKPPNCQIRSKGFSIFPEEDMGSIMERASGKTEN (SEQ ID NO:204).

A polypeptide comprising the amino acid sequence of:
KPVCGNGRLEGNEICDCGTEAQCGPASCCDFRTCVLKDGAKCYKGLCCKDCQILQSGV
ECRPKAHPECDIAENCNGSSPECGPDITLINGLSCKNNKFICYDGDCHDLDARCESVFGK
GSRNAPFACYEEIQSQSDRFGNCGRDRNNKYVFCGWRNLICGRLVCTYPTRKPFHQENG
DVIYAFVRDSVC (SEQ ID NO:205).

A polypeptide comprising the amino acid sequence of:

KPVCGNGRLEGNEICDCGTEAQCGPASCCDFRTCVLKDGAKCYKGLCCKDCQILQSGV ECRPKAHPECDIAENCNGSSPECGPD (SEQ ID NO:206).

A polypeptide comprising the amino acid sequence of: GLSCKNNKFICYDGDCHDLDARCESVFGKGSRNAPFACYEEIQSQSDRFGNCGRDRNNK YVFCGWRNLICGRLVCTYPTRKPFHQENGDVIYAFVRDSVC (SEQ ID NO:207).

A polypeptide comprising the amino acid sequence of: PSSESKSEGSTQTYASQSSSEGSTQTYAGQTRSESSSQADTSKSKSEDSAEAYTSRSKSQD STQTQSSSN (SEQ ID NO:208).

Please substitute the following paragraphs on page 245, beginning at line 20 through to page 246, line 2:

The cDNA of Clone 338116_174-1-1-0-B10-F (SEQ ID NO:71) encodes the protein of SEQ ID NO:72, herein referred as Short Histone Deacetylase (SHDAC), comprising the amino acid sequence: MGPHLHLCLCVPDLRSLRVCVSLWSVHHRPHESLAREEALTALGKLLYLLDGMLDGQV NSGIAATPASAAAATLDVAVRRGLSHAAQRLLCVALGQLDRPPDLAHDGRSLWLNIRG KEAAALSMFHVSTPLPVMTGGFLSCILGLVLPLAYGFQPDLVLVALGPGHGLQGPHXAL LAAMLRGLAGGRVLALLEENSTPQLAGILARVLNGEAPPSLGPSSVASPEDVQALMYLR GQLEPQWKMLQCHPHLVA (SEQ ID NO:72), is encoded by the cDNA clone 338116_174-1-1-0-B10-F (SEQ ID:71). The protein of SEQ ID NO:72 is a novel variant of histone deacetylase (HDAC). Accordingly, it will be appreciated that all characteristics and uses of the polypeptide of SEQ ID NO:72 described throughout the present application also pertain to the polypeptide encoded by a nucleic acid included in clone 338116_174-1-1-0-B10-F. In addition, it will be appreciated that all characteristics and uses of the nucleic acid of SEQ ID NO:71 described throughout the present application also pertain to the nucleic acid included in clone 338116_174-1-1-0-B10-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:71, SEQ ID NO:72, and Clone 338116_174-1-1-0-B10-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

The protein of SEQ ID:72 contains one potential transmembrane segment (position 130 to 150), and a signal peptide (position 1: MGPHLHLCLCVPDLRSL (SEQ ID NO:209)). The protein of SEQ ID:72 is highly expressed in placenta and salivary glands.

Please substitute the following paragraph on page 252, beginning at line 19:

The protein of SEQ ID NO:74, herein referred as short Paraplegin , comprising the amino acid sequence:

MAVLLLLLRALRRGPGPGPRPLWGPGPAWSPGFPARPGRGRPYMASRPPGDLAEAGGR
ALQSLQLRLLTPTFEGINGLLLKQHLVQNPVRLWQLLGGTFYFNTSRLKQKNKEKDKSK
GKAPEEDEGIFI (SEQ ID NO:74), is encoded by the cDNA of clone 500716683_204-24-2-0-D12-F (SEQ ID NO:73). Accordingly, it will be appreciated that all characteristics and uses of the polypeptide of SEQ ID NO:74 described throughout the present application also pertain to the polypeptide encoded by a nucleic acid included in clone 500716683_204-24-2-0-D12-F. In addition, it will be appreciated that all characteristics and uses of the nucleic acid of SEQ ID NO:73 described throughout the present application also pertain to the nucleic acid included in clone 500716683_204-24-2-0-D12-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:73, SEQ ID NO:74, and Clone 500716683_204-24-2-0-D12-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 256, beginning at line 36 through to page 257, line 16:

The protein of SEQ ID NO:76, herein referred as Ketothiolase (KT), comprising the amino acid sequence:

MMGVFVVAAKRTPFGAYGGLLKDFTATDLSEFAAKAALSAGKVSPETVDSVIMGNVLQ
SSSDAIYLARHVGLRVGIPKETPALTINRLCGSGFQSIVNGCQEICVKEAEVVLCGGTESM
SQAPYCVRNVRFGTKLGSDIKLEDSLWVSLTDQHVQLPMAMTAENLAVKHKISREECD
KYALQSQQRWKAANDAGYFNDEMAPIEVKTKKGKQTMQVDEHARPQTTLEQLQKLPP
VFKKDGTVTAGNASGVADGAGAVIIASEDAVKKHNFTPLARIVGYFVSGCDPSIMGIGP

VPAISGALKKAGLSLKDMDLVEVNEAFAPQYLAVERSLDLDISKTNVNGGAIALGHPLG GSGSRITAHLVHELRRRGGKYAVGSACIGGGQGIAVIIQSTA(SEQ ID NO:76), is encoded by the cDNA of clone 500760207_205-58-4-0-H6-F (SEQ ID NO:75). Accordingly, it will be appreciated that all characteristics and uses of the polypeptide of SEQ ID NO:76 described throughout the present application also pertain to the polypeptide encoded by the human cDNA of clone 500760207_205-58-4-0-H6-F. In addition, it will be appreciated that all characteristics and uses of the nucleic acid of SEQ ID NO:75 described throughout the present application also pertain to the human cDNA of clone 500760207_205-58-4-0-H6-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:75, SEQ ID NO:76, and Clone 500760207_205-58-4-0-H6-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraphs on page 261, beginning at line 36 through to page 262, line 25:

The cDNA of clone 122421_105-076-4-0-H1-F (SEQ ID NO:77) encodes the protein of SEQ ID NO:78, comprising the amino acid sequence:
MAAALFVLLGFALLGTHGASGAAGTVFTTVEDLGSKILLTCSLNDSATEVTGHRWLKGG VVLKEDALPGQKTEFKVDSDDQWGEYSCVFLPEPMGTANIQLHGPPRVKAVKSSEHINE GETAMLVCKSESVPPVTDWAWYKITDSEDKALMNGSESRFFVSSSQGLSELHIENLNME ADPGQYRCNGTSSKGSDQAIITLRVRSHLAALWPFLGIVAEVLVLVTIIFIYEKRRKIEDV LDDDDAGSAPLKSSGQHQNDKGKNVRQRNSS(SEQ ID NO:78). Accordingly, it will be appreciated that all characteristics and uses of the polypeptide of SEQ ID NO:78 described throughout the present application also pertain to the polypeptide encoded by the nucleic acids included in clone 122421_105-076-4-0-H1-F. In addition, it will be appreciated that all characteristics and uses of the nucleic acid of SEQ ID NO:77 described throughout the present application also pertain to the nucleic acids included in clone 122421_105-076-4-0-H1-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:77, SEQ ID NO:78, and Clone 122421_105-076-4-0-H1-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the

fragments.

The protein of SEQ ID NO:78 (BASI2) is a novel polymorphic variant of human basigin. BASI2 displays a signal peptide (MAAALFVLLGFALLGTHG(SEQ ID NO:210)), and two immunoglobulin (Ig) domains (GSKILLTCSLNDSATEVTGHRWLKGGVVLKEDALPGQKTEFKVDSDDQWGEYSCVF (SEQ ID NO:211) and GETAMLVCKSESVPPVTDWAWYKITDSEDKALMNGSESRFFVSSSQGLSELHIENLNME ADGQYRCNGTSS (SEQ ID NO:212)). Furthermore, BASI2 displays three N-glycosylation sites (NDSA (SEQ ID NO:213), NGSE (SEQ ID NO:214), and NGTS (SEQ ID NO:215)). The arginine at position 166 in basigin is changed to leucine in BASI2. Thus, the polymorphic, nonconservative change present in BASI2 is located in the second Ig domain, which is involved in protein-protein interactions. Such a polymorphic change located in the second Ig domain has never been previously reported. Thus, as a novel polymorphic variant of basigin, BASI2 displays similar biological activities as basigin, but displays enhanced kinetic parameters during protein-protein interactions.

Please substitute the following paragraphs on page 265, beginning at line 4:

The cDNA clone 99483_105-016-1-0-D7-F (SEQ ID NO:79) encodes KSPI1, the protein of SEQ ID NO:80, comprising the amino acid sequence: MLPPPRPAAALALPVLLLLLVVLTPPPTGARPSPGPDYLRRGWMRLLAEGEGCAPCRPEE CAAPRGCLAGRVRDACGCCWECANLEGQLCDLDPSAHFYGHCGEQLECRLDTGGDLS RGEVPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHPGPCESGPQIVSH PYDTWNVTGQDVIFGCEVFAYPMASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFEVTG WLQIQAVRPSDEGTYRCLGPMPWVKWRPLLA (SEQ ID NO:80). Accordingly, it will be appreciated that all characteristics and uses of the polypeptide of SEQ ID NO:80 described throughout the present application also pertain to the polypeptide encoded by the nucleic acids included in clone 99483_105-016-1-0-D7-F. In addition, it will be appreciated that all characteristics and uses of the nucleic acid of SEQ ID NO:79 described throughout the present application also pertain to the nucleic acids included in clone 99483_105-016-1-0-D7-F. A

preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:79, SEQ ID NO:80, and Clone 99483_105-016-1-0-D7-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments. Preferred KSPI1 polypeptides for uses in the methods described below include the polypeptides comprising the amino sequence of:

CAPCRPEECAAPRGCLAGRVRDACGCCWECANLEGQLCDLDPSAHFYGHCGEQ LECRLDTGGDLSRGEVPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHP GPC (SEQ ID NO:216) and the polypeptide comprising the amino acid sequence of: VPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHPGPC (SEQ ID NO:217).

The protein of SEQ ID NO:80 (KSPI1) is a 267-amino-acid long protein, and is a new variant of the bA108L7.1 gene (Genbank accession number AL133215). The 255 first amino-acids are identical between the two proteins, but the 12 last amino-acids of KSPI1 are unique. KSPI1 displays a signal peptide (MLPPPRPAAALALPVLLLLLVVLTPPPTGA(SEQ ID NO:218)), a kazal-type serine protease inhibitor (Ki) domain (VPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHPGPC (SEQ ID NO:219)), an Immunoglobulin-like (Ig) domain (QDVIFGCEVFAYPMASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFEVTGWLQIQAVRP SDEGTYRCLG (SEQ ID NO:220)) and an Insulin-like growth factor-binding domain (CAPCRPEECAAPRGCLAGRVRDACGCCWECANLEGQLC (SEQ ID NO:221)). Furthermore, KSPI1 displays homologies with many Insulin-like growth factor-binding proteins (IGFBP) from positions 1 to 255, and highest homology with a well-known IGFBP is obtained with human MAC25.

Please substitute the following paragraph on page 286, beginning at line 18:

The cDNA of clone 651658_181-35-2-0-C8-F (SEQ ID NO:91) encodes the protein of SEQ ID NO:92, comprising the amino acid sequence:

MPSSVSWGILLLAGLCCLVPVSLAEDPQGDAAQKTDTSHHDQDHPTFNKITPNLA EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILESLNFNLTEIPEAQIHE GFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEA

KKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQ
ATTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDI
ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKA
VHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPT
QK (SEQ ID NO:92). Accordingly, it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:92 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in clone 651658_181-35-2-0-C8-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:91 described throughout the present application also pertain to the nucleic acids included in clone 651658_181-35-2-0-C8-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:91 and SEQ ID NO:92. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraphs on page 292, beginning at line 25 through to page 294, line 12:

The cDNA of clone 150011_110-006-3-0-D5-F (SEQ ID:93) encodes an allele of Tissue Factor Pathway Inhibitor-1 (TFPI-1), comprising the nucleotide sequence:
CTCTTTGCTCTAACAGACAGCAGCGACTTTAGGCTGGATAATAGTCAAATTCTTACC
TCGCTCTTTCACTGCTAGTAAGATCAGATTGCGTTTCTTTCAGTTACTCTTCAATCGC
CAGTTTCTTGATCTGCTTCTAAAAGAARAAGTAGAGAAGATAAATCCTGTCTTCAAT
ACCTGGAAGGAAAAACAAAATAACCTCAACTCCGTTTTGAAAAAAACATTCCAAGA
ACTTTCATCAGAGATTTTACTTAGATGATTTACACAATGAAGAAAGTACATGCACTT
TGGGCTTCTGTCCCTGCTGCTTAATCTTGCCCCTGCCCCTCTTAATGCTGATTCTGAG
GAAGATGAAGAACACACAATTATCACAGATACGGAGTTGCCACCACTGAAACTTAT
GCATTCATTTTGTGCATTCAAGGCGGATGATAGCCCATGTAAAGCAATCATGAAAAG
ATTTTTCTTCAATATTTTCACTCGACAGTGCGAAGAATTTATATATGGGGGATGTGAA
GGAAATCAGAATCGATTTGAAAGTCTGGAAGAGTGCAAAAAAATGTGTACAAGAGA
TAMTGCAAACAGGATTATAAAGACAACATTGCAACAAGAAAAGCCAGATTTCTGCT
TTTTGGAAGAAGATCCTGGAATATGTCGAGGTTATATTACCAGGTATTTTTATAACA

ATCAGACAAAACATGTGAACGTTTCAAGTATGGTGGATGCCTGGGCAATATGAACA
ATTTTGAGACACTGGAAGAATGCAAGAACATTTGTGAAGATGGTCCGAATGGTTTCC
AGGTGGATAATTATGGAACCCAGCTCAATGCTGTGAATAACTCCCTGACTCCGCAAT
CAACCAAGGTTCCCAGCCTTTTTGTTACAAAAGAAGGAACAAATGATGGTTGGAAG
AATGCGGCTCATATTTACCAAGTCTTTYTGAACGCCTTCTGCATTCATGCATCCATGT
TCTTTCTAGGATTGGATAGCATTTCATGCCTATGTTAATATTTGTGCTTTTGGCATTTC
CTTAATATTTATATGTATACGTGATGCCTTTGATAGCATACTGCTAATAAAGTTTTAA
TATTTACATGCATAGGAAAAAAAAAAAAAAA (SEQ ID NO:93). Accordingly, it will be appreciated that all characteristics and uses of the polypeptides of SEQ ID NO:94 and polynucleotides of SEQ ID NO:93 described throughout the present application also pertain to the nucleic acids included in Clone 150011_110-006-3-0-D5-F. Clone 150011_110-006-3-0-D5-F is alternatively referred to herein as TFPI-C16Pfs in reference to the nucleotide polymorphism that is a subject of the present invention. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:93, SEQ ID NO:94, and Clone 150011_110-006-3-0-D5-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

The cDNA of clone 500737461_205-43-3-0-E3-F (SEQ ID:95) encodes an allele of Tissue Factor Pathway Inhibitor-1 (TFPI-1), comprising the nucleotide sequence:
CTCTTTGCTCTAACAGACAGCAGCGACTTTAGGCTGGATAATAGTCAAATTCTTACC
TCGCTCTTTCACTGCTAGTAAGATCAGATTGCGTTTCTTTCAGTTACTCTTCAATCGC
CAGTTTCTTGATCTGCTTCTAAAAGAAGAAGTAGAGAAGATAAATCCTGTCTTCAAT
ACCTGGAAGGAAAAACAGAATAACCTCAACTCCGTTTTGAAAAAAACATTCCAAGA
ACTTTCATCAGAGATTTTACTTAGATGATTTACACAATGAAGAAAGTACATGCACTT
TGGGCTTCTGTATGCCTGCTGCTTAATCTTGCCCCTGCCCCTCTTAATGCTGATTCTG
AGGAAGATGAAGAACACACAATTATCACAGATACGGAGTTGCCACCACTGAAACTT
ATGCATTCATTTTGTGCATTCAAGGCGGATGATGGCCCATGTAAAGCAATCATGAAA
AGATTTTTCTTCAATATTTTCACTCGACAGTGCGAAGAATTTATATATGGGGGATGTG
AAGGAAATCAGAATCGATTTGAAAGTCTGGAAGAGTGCAAAAAAATGTGTACAAGA
GATAATGCAAACAGGATTATAAAGACAACATTGCAACAAGAAAAGCCAGATTTCTG

CTTTTTGGAAGAAGATCCTGGAATATGTCGAGGTTATATTACCAGGTATTTTTATAAC
AATCAGACAAAACAGTGTGAACGTTTCAAGTATGGTGGATGCCTGGGCAATCAACA
ATTTTGAGACACTGGAACAATGCAAGAACATTTGTGAAGATGGTCCGAATGGTTTCC
AGGTGGATAATTATGGAACCCAGCTCAATGCTGTGAATAACTCCCTGACTCCGCAAT
CAACCAAGGTTCCCAGCCTTTTTGAATTTCACGGTCCCTCATGGTGTCTCACTCCAGC
AGACAGAGGATTGTGTCGTGCCAATGAGAACAGATTCTACTACAATTCAGTCATTGG
GAAATGCCGCCCATTTAAGTACAGTGGATGTGGGGGAAATGAAAACAATTTTACTTC
CAAACAAGAATGTCTGAGGGCATGTAAAAAAGGTTTCATCCAAAGAATATCAAAAG
GAGGCCTAATTAAAACCAAAAGAAAAAGAAAGAAGCAGAGAGTGAAAATAGCATA
TGAAGAAATTTTTGTTAAAAATATGTGAATTTGTTATAGCAATGTAACATTAATTCTA
CTAAATATTTTATATGAAATGTTTCACTATGATTTTCTATTTTTCTTCTAAAATGCTTT
TAATTAATATGTTCATTAAATTTTCTATGCTTATTGCAAAAAAAAAAAAAAAA (SEQ ID NO:95). Accordingly, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:95 and polypeptides of SEQ IDNO:96 described throughout the present application also pertain to the nucleic acids included in Clone 500737461_205-43-3-0-E3-F. Clone 500737461_205-43-3-0-E3-F is alternatively referred to herein as TFPI-M162Qfs in reference to the nucleotide polymorphism that is a subject of the present invention. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:95, SEQ ID NO:96, and Clone 500737461_205-43-3-0-E3-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 297, beginning at line 14:

The cDNA of clone 479155_174-4-4-0-C8-F (SEQ ID NO:99) encodes the protein of SEQ ID NO:100 comprising the amino acid sequence
MIVKGVASRTVVSRPFPGNWLFSSIQLTDDQGPVLMTTVAMPVFSKQNETRSKGILLGV
VGTDVPVKELLKTIPKYKLGIHGYAFAITNNGYILTHPELRLLYEEGKKRRKPNYSSVDLS
EVEWEDRDDVLRNAMVNRKTGKFSMEVKKTVDKGVHFSQTFLLLNLKQTTVKN (SEQ ID NO:100). Accordingly it will be appreciated that all characteristics and uses of polypeptides

of SEQ ID NO:100 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 479155_174-4-4-0-C8-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:99 described throughout the present application also pertain to the nucleic acids included in Clone 479155_174-4-4-0-C8-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:99, SEQ ID NO:100, and Clone 479155_174-4-4-0-C8-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 298, beginning at line 34 through to page 299, line 20:

The cDNA of Clone 586587_181-9-2-0-C5-F (SEQ ID NO: 101) encodes hABC of SEQ ID NO:102, comprising the amino acid sequence:
MACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKA
MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDT
SMKDMRKVLRTLQQIKKSSSRGDKRHFLNWQKGLKPLPQALL(SEQ ID NO:102).
Accordingly, it will be appreciated that all characteristics and uses of the polypeptides of SEQ ID NO:102 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 586587_181-9-2-0-C5-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NOs:101 described throughout the present application also pertain to the nucleic acids included in Clone 586587_181-9-2-0-C5-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:102, SEQ ID NO:101, and Clone 586587_181-9-2-0-C5-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

hABC is a novel splice variant of the ATP-binding cassette 1. As a splice variant, hABC is only 162 amino-acid long whereas ABCA1 is 2261 amino acid long. hABC displays 100% identity with ABCA1 over its 140 amino-terminal residues, whereas the 22 carboxyl-terminal amino acids are unique to hABC. hABC does not display the Walker A and B motifs nor the active

transport signature. The 140 common amino acids correspond to the cytoplasmic amino-terminal tail of ABCA1 that plays a role in cholesterol-binding. Furthermore, hABC displays one transmembrane domain (TCQLLLEVAWPLFIFLILISV(SEQ ID NO:222)) and a "positive-hydrophobic-polar" signal peptide that is required for translocation to the plasma membrane. Moreover, the hABC splice variant is specifically expressed in liver cells. Thus, hABC plays an important role in clearing HDL from the bloodstream by binding to HDL-cholesterol, thus allowing HDL-cholesterol import to liver cells where lipids are catabolized and excreted.

Please substitute the following paragraphs on page 299, beginning at line 32 through to page 300, line 6:

A further embodiment of the invention is directed to a composition comprising a polynucleotide sequence that yields an RNA that is complementary to a polynucleotide sequence encoding a hABC polypeptide fragment. Preferred such a polynucleotide sequence is the polynucleotide sequence that yields an RNA that is complementary to GAGGGGACAAACGCCATTTCCTCAACTGGCAGAAGGGACTGAAGCCTCTCCCTCAA GCCCTTTTA (SEQ ID NO:223).

A further embodiment of the invention is directed to compositions comprising an antibody directed against a hABC polypeptide or against a hABC polypeptide fragment having the same biological activity. Preferably, the antibody specifically binds to the hABC polypeptide or and not to the ABCA1 polypeptide. Even more preferably, the antibody recognizes the LQQIKKSSSRGDKRHFL (SEQ ID NO:224) amino-acid sequence or the RHFLNWQKGLKPLP (SEQ ID NO:225) amino-acid sequence.

Please substitute the following paragraph on page 302, beginning at line 4:

The cDNA of Clone 620315_188-13-1-0-G12-F (SEQ ID NO: 103) encodes MOBP-81h of SEQ ID NO:104, comprising the amino acid sequence: MSQKPAKEGPRLSKNQKYSEHFSIHCCPPFTFLNSKKEIVDRKYSICKSGCFYQKKEEDW ICCACQKTRLKRKIRPTPKKK (SEQ ID NO:104). Accordingly, it will be appreciated that all characteristics and uses of the polypeptides of SEQ ID NO:104 described throughout the present

application also pertain to the polypeptides encoded by the nucleic acids included in Clone 620315_188-13-1-0-G12-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NOs:103 described throughout the present application also pertain to the nucleic acids included in Clone 620315_188-13-1-0-G12-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:104, SEQ ID NO:103, and Clone 620315_188-13-1-0-G12-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 304, beginning at line 11:

The cDNA of Clone 646477_181-19-2-0-F4-F (SEQ ID NO:105) encodes novel Apolipoprotein H (NAPOH) of SEQ ID NO:106, comprising the amino acid sequence: MISPVLILFSSFLCHVAIAGRTCPKPDDLPFSTVVPLKTFYEPGEEITYSCKPGYVSRGGMR KFICPLTGLWLINTLKCTPRVCPFAGILENGAVRYTTFEYPNTISFSCNTGFYLNGADSAK CTEEGKWSPELPVCAPIICPPPSIPTFATLRVYKPSAGNNSLYRDTAVFECLPQHAMFGND TITCTTHGNWTKLPECREVKCPFPSRPDNGFVNYPAKPTLYYKDKATFGCHDGYSLDGP EEIECTKLGNWSAMPSCKASCKVPVKKATVVYQGERVKIQEKFKNGMLHGDKVSFFCK NKEKKCSYTEDAQCIDGTIEVPKCFKEHSSLAFWKTDASDVKPC (SEQ ID NO:106). Accordingly, it will be appreciated that all characteristics and uses of the polypeptides of SEQ ID NO:106 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 646477_181-19-2-0-F4-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:105 described throughout the present application also pertain to the nucleic acids included in Clone 646477_181-19-2-0-F4-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:105, SEQ ID NO:106, and Clone 646477_181-19-2-0-F4-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 313, beginning at line 29 through to page 314, line 8:

The cDNA of Clone 231462_117-065-1-0-G11-F (SEQ ID NO:109) encodes the 386 amino acid long polypeptide, DROCK2, of SEQ ID NO:110 comprising the amino acid sequence:

MCLLLSCPCHPSAHGQSMWIERTSFVTAYKLPGILRWFEVVHMSQTTISPLENAIETMST
ANEKILMMINQYQSDETLPINPLSMLLNGIVDPAVMGGFAKYEKAFFTEEYVRDHPEDQ
DKLTHLKDLIAWQIPFLGAGIKIHEKRVSDNLRPFHDRMEECFKNLKMKVEKEYGVREM
PDFDDRRVGRPRSMLRSYRQMSIISLASMNSDCSTPSKPTSESFDLELASPKTPRVEQEEPI
SPGSTLPEVKLRRSKKRTKRSSVVFADEKAAAESDLKRLSRKHEFMSDTNLSEHAAIPLK
ASVLSQMSFASQSMPTIPALALSVAGIPGLDEANTSPRLSQTFLQLSDGDKKTLTRKKVN
QFFKTMLASKSAEEGKQIPDSLSTDL (SEQ ID NO:110). Accordingly, it will be appreciated that all characteristics and uses of polypeptides of SEQ ID NO:110 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 231462 117-065-1-0-G11-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:109 described throughout the present application also pertain to the nucleic acids included in Clone 231462 117-065-1-0-G11-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:109, SEQ ID NO:110, and Clone 231462 117-065-1-0-G11-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 317, beginning at line 21 through to page 318, line 1:

The cDNA of clone 500723589_205-34-3-0-G4-F (SEQ ID NO:111) encodes Novel 17 beta-hydroxysteroid dehydrogenase type 2 (NBHSD2) of SEQ ID NO:112, comprising the amino acid sequence:

MSTFFSDTAWICLAVPTVLCGTVFCKYKKSSGQLWSWMVCLAGLCAVCLLILSPFWGLI
LFSVSCFLMYTYLSGQELLPVDQKAVLVTGGDCGLGHALCKYLDELGFTVFAGVLNEN
GPGAEELRRTCSPRLSVLQMDITKPVQIKDAYSKVAAMLQDRGLWAVINNAGVLGFPTD

GELLLMTDYKQCMAVNFFGTVEVTKTFLPLLRKSKGRLVNVSSMGGGAPVERLASYGS SKAAVTMFSSVMRLELSKWGIKVASIQPGGFLTNIAGTSDKWEKLEKDILDHLPAEVQE DYCQDYILAQRNFLLLINSLASKDFSPVLRDIQHAILAKSPFAYYTPGKGAYLWICLAHYL PIGIYDYFAKRHFGQDKPMPRALRMPNYKKKAP (SEQ ID NO:112). Accordingly, it will be appreciated that all characteristics and uses of the polypeptides of SEQ ID NO:112 described throughout the present application also pertain to the polypeptides encoded by the nucleic acids included in Clone 500723589_205-34-3-0-G4-F. In addition, it will be appreciated that all characteristics and uses of the polynucleotides of SEQ ID NO:111 described throughout the present application also pertain to the nucleic acids included in Clone 500723589_205-34-3-0-G4-F. A preferred embodiment of the invention is directed toward the compositions of SEQ ID NO:111, SEQ ID NO:112, and clone 500723589_205-34-3-0-G4-F. Also preferred are polypeptide fragments having a biological activity as described herein and the polynucleotides encoding the fragments.

Please substitute the following paragraph on page 343, beginning at line 37 through to page 344, line 13:

Proteins or other molecules interacting with a polypeptide of the present invention, can also be found using affinity columns which contain the GENSET protein, or a fragment thereof. The GENSET protein, or a fragment thereof, may be attached to the column using conventional techniques including chemical coupling to a suitable column matrix such as agarose, ~~Affi-Gel®~~ AFFI-GEL, or other matrices familiar to those of skill in art. In some embodiments of this method, the affinity column contains chimeric proteins in which the GENSET protein, or a fragment thereof, is fused to glutathion S transferase (GST). A mixture of cellular proteins or pool of expressed proteins as described above is applied to the affinity column. Proteins or other molecules interacting with the GENSET protein, or a fragment thereof, attached to the column can then be isolated and analyzed on 2-D electrophoresis gel as described in Ramunsen et al., (1997), Electrophoresis, 18: 588-598, the disclosure of which is incorporated by reference. Alternatively, the proteins retained on the affinity column can be purified by electrophoresis based methods and sequenced. The same

method can be used to isolate antibodies, to screen phage display products, or to screen phage display human antibodies.

Please substitute the Sequence Listing submitted by Applicants on April 22, 2002, with the accompanying Sequence Listing (pages 1-153) on CD-ROM.